SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root
Transcriptional Factor

<130> 1263

<150> US 60/238,292
<151> 2000-10-05

<160> 2

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1280
<212> DNA
<213> Zea mays

<220>
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<400> 1

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tcctcccttg ggaaacctgc tgcctttgag ctttcttctt cgagagctcc caccagatct     180
cctcctcctt accttctttg gcacgttcgg cggcgcgcgc ggagaaagat agatcccgcc     240
atcgtcgtcg tcggtccttg cttccgatcg gagggccaca accacaacct ctcgctccat     300
agcgtgcaag cgcgagccag ggtcaagaag agagctagct agctataggc cggagatcg      359
atg ggg agg gga aag atc gtg atc cgc agg atc gat aac tcc acg agc        407
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
 1               5                  10                  15

cgg cag gtg acc ttc tcc aag cgc cgg aac ggg atc ttc aag aag gcc       455
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
            20                  25                  30

aag gag ctc gcc atc ctc tgc gat gcg gag gtc ggc ctc gtc atc ttc       503
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
        35                  40                  45

tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca       551
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
    50                  55                  60

gtt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca       599
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
65                  70                  75                  80

aat ccc aac tcg gag ctt aag ttt tgg caa agg gag gca gca agc ttg       647
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
                85                  90                  95
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aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga      695
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
            100                 105                 110

gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat      743
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
        115                 120                 125

caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc      791
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
    130                 135                 140

ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac      839
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
145                 150                 155                 160

caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa      887
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
                165                 170                 175

aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga      935
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
            180                 185                 190

gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc      983
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
        195                 200                 205

aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat     1031
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
    210                 215                 220

aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca     1079
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
225                 230                 235                 240

tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg          1132
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aagagatgat actcagagaa agacatattt gtggcaggga gatttgagat atgaacttat  1192
aaatgtaatg caaataattt tcagaccgga atggggtcgt ggaattcaga ggatgattgc  1252
tttctaaaaa aaaaaaaaaa aaaaaaaa                                     1280
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<211> 240
<212> PRT
<213> Zea mays

<400> 2

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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
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Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
        35                  40                  45
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
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50 55 60
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
65 70 75 80
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
85 90 95
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
100 105 110
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
115 120 125
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
130 135 140
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
145 150 155 160
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
165 170 175
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
180 185 190
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
195 200 205
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
210 215 220
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
225 230 235 240